

**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions and listings of the claims in the application.

**LISTING OF CLAIMS:**

1. (Currently Amended) A method of tracking the spread of infectious bacteria, comprising:
  - obtaining a plurality of bacterium samples from a plurality of patients or objects at a plurality of different physical locations;
  - performing DNA sequencing on a first region of deoxyribonucleic acid from each bacterium sample, the first region consisting essentially of a variable number of tandem repeats (VNTRs) region;
  - storing in a database for each of the plurality of bacterium samples: a) the nucleotide sequence data from the first sequenced region of each bacterium sample, and b) [[a]] the physical location of the patient or object from which each bacterium sample was obtained;
  - comparing the nucleotide sequence data stored in the database of at least two of the plurality of samples on both a base pair level and a repeat motif level;
  - determining a measure of phylogenetic relatedness between the compared samples based upon differences between the compared nucleotide sequence data;
  - identifying patients infected or objects contaminated with phylogenetically related bacteria based on the phylogenetic relatedness determination;
  - tracking the spread over time of the bacteria based on: a) the identified patients or contaminated objects, and b) the physical locations of the identified patients or objects stored in the database; and
  - providing a warning based on the tracking of the spread of the bacteria wherein the warning allows the recipient of the warning to control the further spread of the bacteria.
2. Canceled.

3. (Currently Amended) The method of claim 1, wherein the database is a centralized database located ~~[[remote]]~~ at a different location from where the sample is obtained.
4. (Previously Presented) The method of claim 1, wherein the database is located in the same location as where the sample is obtained.
5. (Previously Presented) The method of claim 1, wherein the first region that is sequenced is a region having a mutation rate sufficient to differentiate between subspecies to determine phylogenetic relatedness and to track the bacteria.
6. Canceled.
7. (Currently Amended) The method of claim ~~[[6]]~~ 1, wherein the bacterium is *Staphylococcus aureus* and the first region is located in the protein A gene or the coagulase gene.
8. (Currently Amended) The method of claim ~~[[7]]~~ 1, wherein each bacterium sample is obtained from a patient as the patient is admitted to a health care facility and prior to being exposed to patients in the health care facility.
9. Canceled.
10. (Currently Amended) The method of claim 1, further ~~[[including]]~~ comprising:
  - obtaining a medical history from a patient from which at least one of the plurality of bacterium samples was taken;
  - determining an infection risk factor based on the patient's medical history, the infection risk factor being a measure of the patient's risk of acquiring an infection; and
  - taking appropriate infection control measures in accordance with the infection risk factor.

11. (Currently Amended) The method of claim 10, further ~~[[including]]~~ comprising:  
segregating the information contained within the patient's medical history into  
private information and non-private information;  
transmitting the patient's ~~medical history~~ non-private information to the  
database without transmitting the patient's private ~~[[patient]]~~  
information; and  
storing the patient's private ~~[[patient]]~~ information in a ~~[[local]]~~ database at a  
different location ~~the remote~~ from the database ~~[[that]]~~ to which the  
patient's ~~medical history~~ non-private information is transmitted ~~[[to]]~~.
12. (Currently Amended) The method of claim 1, wherein the step of performing  
DNA sequencing comprises either:
- a) sequencing the first region at a ~~[[remote]]~~ physically separate facility and  
transmitting the resulting nucleotide sequence data to the database via a  
computer network; or
  - b) sending each of the plurality of bacterium samples to an infection control  
facility ~~associated with~~ that has access to the database, sequencing the  
first region at the infection control facility, and storing the nucleotide  
sequence data in the database.
13. (Original) The method of claim 1, wherein the first region is identified by a set of  
primers.
14. (Currently Amended) The method of claim 1, wherein the first region is  
amplified prior to DNA sequencing.
15. Canceled.
16. (Currently Amended) The method of claim 1, wherein the step of determining the  
phylogenetic relatedness between ~~[[the]]~~ at least two compared samples ~~[[includes]]~~  
comprises:
- identifying repeat sequences in the nucleotide sequence data from each sample  
~~for each of the compared samples~~; and treating the insertion or deletion  
of a repeat sequence as a single genetic event.

17. (Currently Amended) The method of claim ~~[[16]]~~ 1, wherein the step of determining the phylogenetic relatedness between ~~[[the]]~~ at least two compared samples comprises ~~[[further including]]~~:  
identifying individual single nucleotide polymorphisms in the nucleotide  
sequence data from each sample; and treating an insertion or deletion or  
change of an individual nucleotide as a single genetic event.
- 18-20. Canceled.
21. (Currently Amended) The method of claim 1, wherein the step of determining the phylogenetic relatedness between ~~[[the]]~~ at least two compared samples ~~[[includes]]~~ comprises at least one of:  
comparing a first bacterium sample to other samples obtained from the same  
~~[[facility]]~~ location as where the first bacterium sample was taken,  
thereby determining a local phylogenetic relatedness;  
comparing the first bacterium sample to other samples obtained from the same  
geographical region as where the first bacterium sample was taken,  
thereby determining a regional phylogenetic relatedness; and  
comparing the first bacterium sample to other samples obtained  
globally, thereby determining a global phylogenetic  
relatedness.
22. (Currently Amended) The method of claim 1, wherein the steps of storing  
nucleotide sequence data in a database and tracking the spread of the  
infection further comprises:  
transmitting over a computer network ~~from a remote facility to an infection~~  
~~control server~~ the nucleotide sequence data from the first sequenced  
region of each of the plurality of bacterium samples and the physical  
location of the patient or object from which each bacterium sample is  
taken.

23. (Currently Amended) The method of claim 22, further ~~[[including]]~~ comprising:  
storing in the database a map of the physical location of where the plurality of  
samples were obtained ~~in the database~~; and  
determining the spread of the infection based on the map.
24. (Currently Amended) The method of claim 23, further ~~[[including]]~~ comprising:  
~~[[sensing]]~~ determining, via sensor, the patient's physical location prior to  
transmitting the patient's physical location.
25. (Currently Amended) The method of claim 1, further ~~[[including]]~~ comprising:  
determining the virulence of the bacterium by retrieving the virulence data of  
identical or similar bacteria from the database; and  
transmitting over a computer network virulence information to a location  
where the bacterium sample was obtained.
26. (Previously Presented) The method of claim 1, further comprising:  
determining drug resistance and treatment information of the bacterium by  
retrieving drug information data of identical or similar bacteria from  
the database; and  
transmitting over a computer network the drug information data to a location  
where the bacterium sample was obtained.
27. (Currently Amended) The method of claim 1, wherein providing a warning  
~~[[includes]]~~ comprises:  
determining whether a location where each bacterium was obtained has an  
outbreak problem; and  
transmitting over a computer network an outbreak warning to each location  
having an outbreak problem.

28. (Currently Amended) The method of claim 1, further ~~[[including]]~~ comprising:  
    performing DNA sequencing on a second region of ~~the nucleic~~  
        deoxyribonucleic acid of each bacterium sample;  
storing the nucleotide sequence data from the second region of the ~~[[nucleic]]~~  
        deoxyribonucleic acid of each bacterium sample in a database;  
comparing the nucleotide sequence data from the second sequenced region  
        ~~of at least two of the plurality of samples to nucleotide sequence~~  
        data already stored in the database, wherein the determining a  
        measure of phylogenetic relatedness comprises; and  
determining a measure of phylogenetic relatedness based on the comparison of  
    the first and second sequenced regions.
29. (Original) The method of claim 28, wherein the determination of relatedness based  
on the second sequenced region is used to verify the determination of relatedness based  
on the first sequenced region.
30. (Currently Amended) The method of claim 28, further ~~[[including]]~~  
comprising:  
    identifying a first level of subspecies of each bacterium sample based on  
        the first sequenced region; and  
    identifying a second level of subspecies of each bacterium sample based on the  
        second sequenced region.
31. (Currently Amended) The method of claim 28, further ~~[[including]]~~ comprising:  
    tracking the global spread of an infection based on the sequencing and  
        comparing a slowly mutating region of the deoxyribonucleic  
        ~~[[nucleic]]~~ acid; and  
    tracking the local spread of an infection based on the sequencing and  
        comparing a more rapidly mutating region of the deoxyribonucleic  
        ~~[[nucleic]]~~ acid.

32. (Currently Amended) A system for tracking the spread of infectious bacteria, comprising:
- a computer network;
  - a centralized database;
  - a ~~[[remote]]~~ facility, connected to the computer network, ~~the remote facility obtaining~~ where a plurality of bacterium samples from a plurality of patients or objects at a plurality of different locations are obtained;
  - a server connected to the computer network, the server receiving nucleotide sequence data for a first sequenced region of a ~~[[nucleic]]~~ deoxyribonucleic acid from each of the plurality of bacterium samples and a physical location of a patient or object from which each bacterium sample was obtained, the first sequenced region consisting essentially of a variable number of tandem repeats (VNTRs) region;
  - storing in a database for each of the plurality of bacterium samples: a) the nucleotide sequence data from each of the plurality of bacterium samples, and b) the physical location of the patient or object from which each bacterium sample was obtained;
  - accessing the centralized database and comparing the stored nucleotide sequence data of at least two of the plurality of bacterium samples ~~on both a base pair level and a repeat motif level~~;
  - determining a measure of phylogenetic relatedness between the compared samples;
  - identifying patients infected or objects contaminated with phylogenetically related bacteria based on the phylogenetic relatedness determination;
  - tracking the spread over time of the bacteria based on a) the identified patients or objects, and b) and the physical locations of the identified patients or objects stored in the database; and
  - transmitting a warning over the computer network to the ~~[[remote]]~~ facility based on the tracking of the spread of the bacteria, thereby allowing the ~~[[remote]]~~ facility to control ~~[[the]]~~ further spread of the bacterial infection.

33. (Currently Amended) Computer-executable software code stored on a computer-readable medium for performing the method according to claim 1, for performing a method of tracking wherein said spread of infectious bacteria is tracked using [[over]] a computer network, ~~comprising:~~  
obtaining a plurality of bacterium samples from a plurality of patients at a plurality of different locations;  
sequencing a first region of a nucleic acid from each of the plurality of bacterium samples, the first region consisting essentially of a variable number of tandem repeats (VNTRs) region;  
storing in a database: a) the sequence data from the first sequenced region of each bacterium sample, and b) a physical location of a patient or object from which each bacterium sample was obtained;  
comparing the stored sequence data of at least two of the plurality of samples on both a base pair level and a repeat motif level;  
determining a measure of phylogenetic relatedness between the compared samples;  
identifying patients infected or objects contaminated with phylogenetically related bacteria based on the phylogenetic relatedness determination;  
tracking the spread of the bacteria based on the identified patients or objects and the physical locations of the identified patients and objects stored in the database; and  
providing bacterial spread information based on the tracking of the spread of the bacteria, thereby allowing use of the bacterial spread information to further control the spread of the bacteria.
34. (Currently Amended) The method of claim 1, wherein the plurality of bacterium samples are obtained at a ~~facility remote~~ location physically separate from where the DNA sequencing is carried out performed.
35. (Currently Amended) The method of claim 34, wherein the ~~remote facility~~ physically separate location is a health care facility, and the sample of the bacterium is obtained from a patient as the patient is admitted to a health care facility and prior to being exposed to patients in the health care facility.



36. (Currently Amended) The method of claim 1, wherein the sample is obtained at a ~~facility remote~~ location physically separate from where the DNA sequencing, comparing, and determination of a measure of phylogenetic relatedness occurs ~~are carried out~~.
37. Canceled.
38. (Currently Amended) The method according to claim 1, wherein what may be an outbreak of bacterial infection is confirmed or refuted based upon the determination of phylogenetic relatedness ~~infected patients are identified prior to an outbreak of the bacterial infection~~.
- 39-41. Canceled.

42. (Withdrawn) A method of tracking the spread of bacteria, comprising:
  - obtaining a plurality of bacterium samples from a plurality of patients at a plurality of different locations;
  - sequencing a first region of deoxyribonucleic acid from each of the plurality of bacterium samples, the first region consisting essentially of a variable number of tandem repeats (VNTRs) region;
  - storing in a database: a) the sequenced data from each bacterium sample; and b) the location of the each patient;
  - comparing the stored sequence data of at least two of the plurality of bacterium samples on both a base pair level and a repeat motif level;
  - determining the phylogenetic relatedness of the sequence data between the compared samples based on: a) the number of insertions and deletions of individual nucleotides; and b) the number of insertions and deletions of repeat cassettes, wherein a repeat cassette comprises a sequence of nucleotides which repeats in the first region of the deoxyribonucleic acid;
  - tracking the spread over time of the bacteria based on a) the phylogenetic relatedness determination, and b) the physical locations of the patients stored in the database; and
  - providing a warning based on the tracking of the spread of the bacteria wherein the warning allows the recipient of the warning to control the further spread of the bacteria.

43. (Withdrawn) A method of tracking the spread of bacteria, comprising:
- obtaining a plurality of bacterium samples from a plurality of patients at a plurality of different locations;
  - sequencing a first region of deoxyribonucleic acid from each of the plurality of bacterium samples, the first region consisting essentially of a variable number of tandem repeats (VNTRs) region;
  - storing in a database: a) the sequenced data from each bacterium sample; and b) the location of the each patient;
  - comparing the stored sequence data of at least two of the plurality of bacterium samples on both a base pair level and a repeat motif level;
  - determining the phylogenetic relatedness of the sequence data between the compared samples, wherein the insertion or deletion of a repeat cassette is treated as a single genetic event, wherein a repeat cassette comprises a sequence of nucleotides which repeats in the first region;
  - tracking the spread over time of the bacteria based on a) the phylogenetic relatedness determination, and b) the physical locations of the patients stored in the database; and
  - providing a warning based on the tracking of the spread of the bacteria wherein the warning allows the recipient of the warning to control the further spread of the bacteria.
44. (Currently Amended) The system of claim 32, wherein the DNA sequencing occurs at the facility and further wherein the nucleotide sequence data is transmitted over the computer network to the server further comprising:
- ~~sequencing the first region of the nucleic acid for each of the plurality of bacterium samples at the remote facility; and~~
  - ~~transmitting the sequence data to the server over a computer network.~~
45. (New) The system of claim 32, wherein the step of determining the phylogenetic relatedness between at least two compared samples comprises:
- identifying repeat sequences in the nucleotide sequence data from each sample;
  - and treating the insertion or deletion of a repeat sequence as a single genetic event.

46. (New) The system of claim 32, wherein the step of determining the phylogenetic relatedness between at least two compared samples comprises:  
identifying individual single nucleotide polymorphisms in the nucleotide  
sequence data from each sample; and treating the insertion or deletion  
or change of an individual nucleotide as a single genetic event.